RAW SEQUENCE LISTING ERROR REPORT
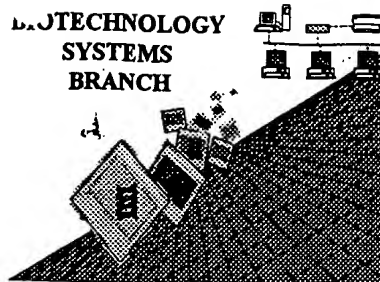
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/936,737_

Source: _PCT/09_

Date Processed by STIC: _10/4/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE __CHECKER VERSION 3.0 PROGRAM__, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/936,937_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWAR

1_____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____Variable Length

Sequence(s)_____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7_____Skipped Sequences
(OLD RULES)

Sequence(s)_____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11_____Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/936,737   DATE: 10/04/2001
                                             TIME: 15:36:11

          Input Set : **A:\ES.txt**
          Output Set: **N:\CRF3\10042001\I936737.raw**   **Does Not Comply**
                                                                Corrected Diskette Needed

        3 <110> APPLICANT: Merck Patent GmbH
        5 <120> TITLE OF INVENTION: Protein for blocking platelet adhesion
        7 <130> FILE REFERENCE: Saratin Sequence
C-->   9 **<140> CURRENT APPLICATION NUMBER: US/09/936,737**
C-->   10 **<141> CURRENT FILING DATE: 2001-09-17**
       12 <160> NUMBER OF SEQ ID NOS: 12
       14 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

      197 <210> SEQ ID NO: 12
      198 <211> LENGTH: 27
      199 <212> TYPE: DNA
      200 <213> ORGANISM: Artificial Sequence
      202 <220> FEATURE:
      203 <223> OTHER INFORMATION: Description of Artificial Sequence: primer10
      205 <400> SEQUENCE: 12
      206 gcatgaattc gaagaacgtg aagattg
E--> 212 - 4 - delete   27

see next page

RAW SEQUENCE LISTING   DATE: 10/23/2001
PATENT APPLICATION: US/09/936,737   TIME: 13:41:08

                Input Set : A:\PTO.AMC.txt
                Output Set: N:\CRF3\10232001\I936737.raw

```
 70              35                   40                   45
 72 Val Asn Lys Glu Cys Tyr Tyr Asn Val Val Asp Gly Glu Glu Leu Asp
 73      50              .       55                   60
 75 Gln Glu Lys Phe Val Val Asp Glu Asn Phe Thr Glu Asn Tyr Leu Thr
 76  65                      70                   75                   80
 78 Asp Cys Glu Gly Lys Asp Ala Gly Asn Ala Ala Gly Thr Gly Asp Glu
 79              85                   90                   95
 81 Ser Asp Glu Val Asp Glu Asp
 82              100
 86 <210> SEQ ID NO: 3
 87 <211> LENGTH: 23
 88 <212> TYPE: DNA
 89 <213> ORGANISM: Artificial Sequence
 91 <220> FEATURE:
 92 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
 93       primer01
 95 <400> SEQUENCE: 3
 96 gargarmggg argaytgttg gac                                    23
 99 <210> SEQ ID NO: 4
100 <211> LENGTH: 23
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
106       primer02
108 <400> SEQUENCE: 4
109 gargarmggg argaytgctg gac                                    23
112 <210> SEQ ID NO: 5
113 <211> LENGTH: 24
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Artificial Sequence: primer03
120 <400> SEQUENCE: 5
121 gcatcgatgg aagaacgtga agac                                   24
124 <210> SEQ ID NO: 6
125 <211> LENGTH: 23
126 <212> TYPE: DNA
127 <213> ORGANISM: Artificial Sequence
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Description of Artificial Sequence: primer04
132 <400> SEQUENCE: 6
133 tagcgctttt gacgtcgtcg tca                                    23
136 <210> SEQ ID NO: 7
137 <211> LENGTH: 26
138 <212> TYPE: DNA
139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
142 <223> OTHER INFORMATION: Description of Artificial Sequence: primer05
```

W--> 96 (handwritten) → see item 9 on Error Summary Sheet

W--> 109 (handwritten) → item 9

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/936,737**   DATE: 10/04/2001
TIME: 15:36:12

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\10042001\I936737.raw**

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:96 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:96 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:96 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:109 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:109 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:212 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:12